

AMENDMENTS TO THE CLAIMS

1. (Original) A process for preparing amino acids selected from the group of methionine, homoserine and lysine in transgenic organisms, wherein the process comprises the following steps:
 - a) introduction of a nucleic acid sequence which codes for a threonine-degrading protein or lysine-degrading protein or codes for a threonine-degrading protein and lysine-degrading protein, or
 - b) introduction of a nucleic acid sequence which increases threonine degradation or lysine degradation or threonine degradation and lysine degradation in the transgenic organisms, and
 - c) expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.
2. (Original) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:
 - a) introduction of a nucleic acid sequence which codes for a threonine-degrading protein which comprises the following consensus sequence
$$H[x]_2G[X]R[X]_{19}D[X]_7K[X]_{27}G, \text{ or}$$
$$HXDGAR[X]_3A[X]_{15}D[X]_4CXSK[X]_4PXGS[X]_3G[X]_7A[X]_4K[X]_2GGGXRQXG$$
or
 - b) introduction of a nucleic acid sequence which increases threonine degradation in the transgenic organism, and
 - c) expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.

3. (Original) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:
- introduction of a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

G[X]₄GIM[X]₄₅M[X]₂RK[X]₂M[X]₁₁GGXG[X]₃E[X]₂E[X]₃W, or
 LG[X]₉LVEYGG[X]₃GIMGXVA[X]₉G[X]₃GXIP[X]₂₄MHXRK[X]₂M[X]₆F[X]₃PGG
 XGTXEE[X]₂E[X]₂TW[X]₂IG[X]₃KP[X]₄N[X]₃FY[X]₁₄F, or
 - introduction of a nucleic acid sequence which increases lysine degradation in the transgenic organisms, and
 - expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.
4. (Original) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:
- introduction of a nucleic acid sequence which codes for a threonine-degrading protein which comprises the following consensus sequence

H[X]₂G[X]R[X]₁₉D[X]₇K[X]₂₇G, or
 HXDGAR[X]₃A[X]₁₅D[X]₄CXSK[X]₄PXGS[X]₃G[X]₇A[X]₄K[X]₂GGGXRQXG

and introduction of a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

G[X]₄GIM[X]₄₅M[X]₂RK[X]₂M[X]₁₁GGXG[X]₃E[X]₂E[X]₃W, or
 LG[X]₉LVEYGG[X]₃GIMGXVA[X]₉G[X]₃GXIP[X]₂₄MHXRK[X]₂M[X]₆F[X]₃PGG
 XGTXEE[X]₂E[X]₂TW[X]₂IG[X]₃KP[X]₄N[X]₃FY[X]₁₄F, or

- b) introduction of a nucleic acid sequence which codes for proteins which increase threonine degradation and lysine degradation in the transgenic organisms, and
 - c) expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.
5. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein there is introduction in process step (a) as set forth in ~~claims 1 to 4~~ claim 1 of a nucleic acid sequence which is selected from the group of nucleic acid sequences:
- i) of a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25;
 - ii) of a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26, and
 - iii) of a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25; which codes for polypeptides having the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino acid level, with a negligible reduction in the biological activity of the polypeptides.
6. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claim 1 or 2 or claims 4 and 5~~ claim 1, wherein there is introduction in process step (a) of a nucleic acid sequence which is selected from the group of nucleic acid sequences:

- i) of a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10;
 - ii) of a derivative of the nucleic acid sequence which is obtained by back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10 and which has at least 70% homology at the amino acid level with the aforementioned amino acid sequences, with a negligible reduction in the biological activity of the polypeptides.
7. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 6~~ claim 1, wherein the transgenic organism is cultivated and harvested after introduction and expression of the nucleic acid.
8. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 7~~ claim 1, wherein the amino acid is isolated from the organism or the culture medium or the organism and the culture medium.
9. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 9~~ claim 1, wherein the essential amino acid methionine is involved.
10. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 10~~ claim 1, wherein the transgenic organism is a microorganism or a plant.
11. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 11~~ claim 10, wherein the transgenic organism is a microorganism selected from the group of genera Corynebacterium, Brevibacterium, Escherichia, Bacillus, Rhodotorula, Hansenula, Schizosaccharomyces, Saccharomyces, Candida, Claviceps or Flavobacterium.

12. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 12~~ claim 10, wherein the transgenic organism is a plant selected from the group of crop plants.
13. (Original) A process for preparing amino acids in transgenic organisms as claimed in claim 12, wherein the transgenic organism is a plant selected from the group of peanut, oilseed rape, canola, sunflower, safflower, olive, sesame, hazelnut, almond, avocado, bay, pumpkin, lettuce, flax, soybean, pistachio, borage, corn, wheat, rye, oats, millet, triticle, rice, barley, cassava, potato, sugar beet, feed beet, aubergine, tomato, pea, alfalfa and perennial grasses and feed crops.
14. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 14~~ claim 1, wherein the nucleic acid sequence is derived from a eukaryote.
15. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 15~~ claim 1, wherein the nucleic acid sequence is derived from the genus *Saccharomyces*.
16. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 16~~ claim 1, wherein the nucleic acid sequence is for introduction and for expression incorporated into a nucleic acid construct or a vector.
17. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in ~~claims 1 to 17~~ claim 1, wherein additionally biosynthesis genes of the amino acid prepared in the process are introduced into the organism.
18. (Currently amended) A nucleic acid construct comprising a nucleic acid sequence ~~as set forth in claims 2 to 6~~ selected from the group consisting of:
 - a) a nucleic acid which codes for a threonine-degrading protein which comprises the following consensus sequence H[x]₂G[x]R[x]₁₉D[x]₇K[x]₂₇G, or
HXDGAR[x]₃A[x]₁₅D[x]₄CXSK[x]₄PXGS[x]₃G[x]₇A[x]₄K[x]₂GGGXRXGX

- b) a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

G[X]₄GIM[X]₄₅M[X]₂RK[X]₂M[X]₁₁GGXG[X]₃E[X]₂E[X]₃W, or

LG[X]₉LVYGG[X]₃GIMGXVA[X]₉G[X]₃GXIP[X]₂₄MHXRK[X]₂M[X]₆F[X]₃PGG

XGTXEE[X]₂E[X]₂TW[X]₂IG[X]₃KP[X]₄N[X]₃FY[X]₁₄F;

- c) a nucleic acid sequence which comprises the nucleic acid sequence under (a) and the nucleic acid sequence under (b);
- d) a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25;
- e) a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26;
- f) a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25; which codes for polypeptides having the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino acid level, with a negligible reduction in the biological activity of the polypeptides;
- g) a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10; and

h) a derivative of the nucleic acid sequence which is obtained by back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10 and which has at least 70% homology at the amino acid level with the aforementioned amino acid sequences, with a negligible reduction in the biological activity of the polypeptides;

wherein the nucleic acid sequence which is functionally linked to one or more regulatory signals.

19. (Currently amended) A vector comprising a nucleic acid sequence ~~as set forth in claims 2 to 6 or a nucleic acid construct as set forth in claim 18~~ selected from the group consisting of:

a) a nucleic acid which codes for a threonine-degrading protein which comprises the following consensus sequence H[X]₂G[X]R[X]₁₉D[X]₇K[X]₂₇G, or HXDGAR[X]₃A[X]₁₅D[X]₄CXSK[X]₄PXGS[X]₃G[X]₇A[X]₄K[X]₂GGGXRXGXG

b) a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

G[X]₄GIM[X]₄₅M[X]₂RK[X]₂M[X]₁₁GGXG[X]₃E[X]₂E[X]₃W, or

LG[X]₉LVEYGG[X]₃GIMGXVA[X]₉G[X]₃GXIP[X]₂₄MHXRK[X]₂M[X]₆F[X]₃PGG

XGTXEE[X]₂E[X]₂TW[X]₂IG[X]₃KP[X]₄N[X]₃FY[X]₁₄F;

c) a nucleic acid sequence which comprises the nucleic acid sequence under (a) and the nucleic acid sequence under (b);

d) a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25;

- e) a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26;
- f) a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25; which codes for polypeptides having the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino acid level, with a negligible reduction in the biological activity of the polypeptides;
- g) a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10; and
- h) a derivative of the nucleic acid sequence which is obtained by back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10 and which has at least 70% homology at the amino acid level with the aforementioned amino acid sequences, with a negligible reduction in the biological activity of the polypeptides.
20. (Currently amended) A transgenic prokaryotic or eukaryotic organism comprising at least one nucleic acid sequence ~~as set forth in claims 2 to 6 or at least one nucleic acid construct as set forth in claim 18 or at least one vector as set forth in claim 19~~ selected from the group consisting of:

- a) a nucleic acid which codes for a threonine-degrading protein which comprises the following consensus sequence H[x]₂G[X]R[X]₁₉D[X]₇K[X]₂₇G, or HXDGAR[X]₃A[X]₁₅D[X]₄CXSK[X]₄PXGS[X]₃G[X]₇A[X]₄K[X]₂GGGXRXGXG;
- b) a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence
G[X]₄GIM[X]₄₅M[X]₂RK[X]₂M[X]₁₁GGXG[X]₃E[X]₂E[X]₃W, or
LG[X]₉LVYGG[X]₃GIMGXVA[X]₉G[X]₃GXIP[X]₂₄MHXRK[X]₂M[X]₆F[X]₃PGG
XGTXEE[X]₂E[X]₂TW[X]₂IG[X]₃KP[X]₄N[X]₃FY[X]₁₄F;
- c) a nucleic acid sequence which comprises the nucleic acid sequence under (a) and the nucleic acid sequence under (b);
- d) a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25;
- e) a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26;
- f) a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25; which codes for polypeptides having the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino acid level, with a negligible reduction in the biological activity of the polypeptides;

- g) a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10; and
- h) a derivative of the nucleic acid sequence which is obtained by back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10 and which has at least 70% homology at the amino acid level with the aforementioned amino acid sequences, with a negligible reduction in the biological activity of the polypeptides.
21. (Original) A transgenic prokaryotic or eukaryotic organism as claimed in claim 20, which is a microorganism or a plant.
22. (Original) A transgenic prokaryotic or eukaryotic organism as claimed in claim 21, which is a microorganism of the genus *Corynebacterium* or *Brevibacterium*.
23. (Original) A transgenic prokaryotic or eukaryotic organism as claimed in claim 21, which is a plant selected from the group of genus of peanut, oilseed rape, canola, sunflower, safflower, olive, sesame, hazelnut, almond, avocado, bay, pumpkin, lettuce, flax, soybean, pistachio, borage, corn, wheat, rye, oats, millet, triticale, rice, barley, cassava, potato, sugar beet, feed beet, aubergine, tomato, pea, alfalfa and perennial grasses and feed crops.
24. (Currently amended) ~~The use of the transgenic organisms as set forth in claims 20 to 23 or of an amino acid prepared by a process as set forth in claims 1 to 18~~ A process for producing an animal or human food, for producing cosmetics or pharmaceuticals, comprising growing or culturing the transgenic organism of claim 20, recovering the amino acid produced, and formulating the amino acid into an animal or human food, cosmetics or pharmaceuticals.

25. (Original) An amino acid sequence selected from the group of sequences SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10.